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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/047,542

DATE: 06/06/2002

TIME: 10:42:30

Input Set : A:\03090504.app

Output Set: N:\CRF3\06062002\J047542.raw

p.6

3 <110> APPLICANT: LARRICK, JAMES W.  
4 WYCOFF, KEITH L.  
6 <120> TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL  
7 AND BACTERIAL DISEASES  
9 <130> FILE REFERENCE: 030905.0004.CIP1  
11 <140> CURRENT APPLICATION NUMBER: US 10/047,542  
12 <141> CURRENT FILING DATE: 2001-10-26  
14 <150> PRIOR APPLICATION NUMBER: PCT/US01/13932  
15 <151> PRIOR FILING DATE: 2001-04-28  
17 <150> PRIOR APPLICATION NUMBER: 60/200,298  
18 <151> PRIOR FILING DATE: 2000-04-28  
20 <160> NUMBER OF SEQ ID NOS: 101  
22 <170> SOFTWARE: PatentIn Ver. 2.1  
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25 <211> LENGTH: 1596  
26 <212> TYPE: DNA  
27 <213> ORGANISM: Homo sapiens  
29 <400> SEQUENCE: 1

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32 ggaggtcccg tgctggtgac atgcagcacc tcctgtgacc agcccaagtt gttgggcata 180  
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35 tcaacagcta aaaccttcct caccgtgtac tggactccag aacgggtgga actggcacc 360  
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38 ccagctgttg gggagcccgc tgaggtcacg accacggtgc tgggtgaggag agatcaccat 540  
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41 ctgttcagcc ccggggtcct agaggtggac acgcaggga ccgtggtctg ttccctggac 720  
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49 cttatacaca agaaccagac ccgggagctt cgtgtcctgt atggcccccg actggacgag 1200  
50 agggattgtc cgggaaactg gacgtggcca gaaaattccc agcagactcc aatgtgccag 1260  
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68 Leu Gly Ala Leu Phe Pro Gly Pro Gly Asn Ala Gln Thr Ser Val Ser
69 20 25 30
71 Pro Ser Lys Val Ile Leu Pro Arg Gly Gly Ser Val Leu Val Thr Cys
72 35 40 45
74 Ser Thr Ser Cys Asp Gln Pro Lys Leu Leu Gly Ile Glu Thr Pro Leu
75 50 55 60
77 Pro Lys Lys Glu Leu Leu Leu Pro Gly Asn Asn Arg Lys Val Tyr Glu
78 65 70 75 80
80 Leu Ser Asn Val Gln Glu Asp Ser Gln Pro Met Cys Tyr Ser Asn Cys
81 85 90 95
83 Pro Asp Gly Gln Ser Thr Ala Lys Thr Phe Leu Thr Val Tyr Trp Thr
84 100 105 110
86 Pro Glu Arg Val Glu Leu Ala Pro Leu Pro Ser Trp Gln Pro Val Gly
87 115 120 125
89 Lys Asn Leu Thr Leu Arg Cys Gln Val Glu Gly Gly Ala Pro Arg Ala
90 130 135 140
92 Asn Leu Thr Val Val Leu Leu Arg Gly Glu Lys Glu Leu Lys Arg Glu
93 145 150 155 160
95 Pro Ala Val Gly Glu Pro Ala Glu Val Thr Thr Thr Val Leu Val Arg
96 165 170 175
98 Arg Asp His His Gly Ala Asn Phe Ser Cys Arg Thr Glu Leu Asp Leu
99 180 185 190
101 Arg Pro Gln Gly Leu Glu Leu Phe Glu Asn Thr Ser Ala Pro Tyr Gln
102 195 200 205
104 Leu Gln Thr Phe Val Leu Pro Ala Thr Pro Pro Gln Leu Val Ser Pro
105 210 215 220
107 Arg Val Leu Glu Val Asp Thr Gln Gly Thr Val Val Cys Ser Leu Asp
108 225 230 235 240
110 Gly Leu Phe Pro Val Ser Glu Ala Gln Val His Leu Ala Leu Gly Asp
111 245 250 255
113 Gln Arg Leu Asn Pro Thr Val Thr Tyr Gly Asn Asp Ser Phe Ser Ala
114 260 265 270
116 Lys Ala Ser Val Ser Val Thr Ala Glu Asp Glu Gly Thr Gln Arg Leu
117 275 280 285
119 Thr Cys Ala Val Ile Leu Gly Asn Gln Ser Gln Glu Thr Leu Gln Thr
120 290 295 300
122 Val Thr Ile Tyr Ser Phe Pro Ala Pro Asn Val Ile Leu Thr Lys Pro
123 305 310 315 320
125 Glu Val Ser Glu Gly Thr Glu Val Thr Val Lys Cys Glu Ala His Pro
126 325 330 335

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128 Arg Ala Lys Val Thr Leu Asn Gly Val Pro Ala Gln Pro Leu Gly Pro
129           340           345           350
131 Arg Ala Gln Leu Leu Leu Lys Ala Thr Pro Glu Asp Asn Gly Arg Ser
132           355           360           365
134 Phe Ser Cys Ser Ala Thr Leu Glu Val Ala Gly Gln Leu Ile His Lys
135           370           375           380
137 Asn Gln Thr Arg Glu Leu Arg Val Leu Tyr Gly Pro Arg Leu Asp Glu
138 385           390           395           400
140 Arg Asp Cys Pro Gly Asn Trp Thr Trp Pro Glu Asn Ser Gln Gln Thr
141           405           410           415
143 Pro Met Cys Gln Ala Trp Gly Asn Pro Leu Pro Glu Leu Lys Cys Leu
144           420           425           430
146 Lys Asp Gly Thr Phe Pro Leu Pro Ile Gly Glu Ser Val Thr Val Thr
147           435           440           445
149 Arg Asp Leu Glu Gly Thr Tyr Leu Cys Arg Ala Arg Ser Thr Gln Gly
150           450           455           460
152 Glu Val Thr Arg Lys Val Thr Val Asn Val Leu Ser Pro Arg Tyr Glu
153 465           470           475           480
155 Ile Val Ile Ile Thr Val Val Ala Ala Val Ile Met Gly Thr Ala
156           485           490           495
158 Gly Leu Ser Thr Tyr Leu Tyr Asn Arg Gln Arg Lys Ile Lys Lys Tyr
159           500           505           510
161 Arg Leu Gln Gln Ala Gln Lys Gly Thr Pro Met Lys Pro Asn Thr Gln
162           515           520           525
164 Ala Thr Pro Pro
165           530
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169 <211> LENGTH: 3003
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171 <213> ORGANISM: Homo sapiens
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176 tcggggctct gttcccagga cctggcaatg cccagacatc tgtgtccccc tcaaaagtca 180
177 tcctgccccg gggaggtccc gtgctggtga catgcagcac ctccgtgtgac cagcccaagt 240
178 tggtgggcat agagaccccg ttgcctaaaa aggagttgct cctgcctggg aacaaccgga 300
179 aggtgtatga actgagcaat gtgcaagaag atagccaacc aatgtgctat tcaaaactgcc 360
180 ctgatgggca gtcaacagct aaaaccttcc tcaccgtgta ctggactcca gaacgggtgg 420
181 aactggcacc cctccctctt tggcagccag tgggcaagaa ccttacccta cgctgccagg 480
182 tggaggtggg ggcaccccgg gccaacctca ccgtggtgct gctccgtggg gagaaggagc 540
183 tgaaacggga gccagctgtg ggggagcccc ctgaggtcac gaccacggtg ctggtgagga 600
184 gagatcacca tggagccaat ttctcgtgcc gcaactgaact ggacctgcgg cccaaggggc 660
185 tggagctggt tgagaacacc tcggccccct accagctcca gacctttgtc ctgccagcga 720
186 ctcccccaca acttgtcagc ccccggttcc tagaggtgga caagcagggg accgtggtct 780
187 gttccctgga cgggctgttc ccagtcctcg aggccaggt ccacctggca ctgggggacc 840
188 agaggttgaa cccacagtc acctatggca acgactcctt ctggccaag gcctcagtca 900
189 gtgtgaccgc agaggacgag ggcacccagc ggctgacgtg tgcagtaata ctggggaacc 960
190 agagccagga gacactgcag acagtgaaca tctacagctt tccggcgccc aacgtgattc 1020
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192 gagccaaggt gacgtgaat ggggttccag ccagccact gggcccagag gccagctcc 1140
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194 tggccggcca gcttatacac aagaaccaga cccgggagct tcgtgtcctg tatggcccc 1260
195 gactggacga gagggattgt ccgggaaact ggacgtggcc agaaaattcc cagcagactc 1320
196 caatgtgcca ggcttggggg aaccattgc ccgagctcaa gtgtctaaag gatggcactt 1380
197 tcccactgcc catcggggaa tcagtactg tcactcgaga tcttgagggc acctacctct 1440
198 gtcgggccaag gagcactcaa ggggaggtca cccgcaaggt gaccgtgaat gtgctctccc 1500
199 cccggtatga gattgtcatc atcactgtgg tagcagccgc agtcataatg ggcactgcag 1560
200 gcctcagcac gtacctctat aaccgccagc ggaagatcaa gaaatacaga ctacaacagg 1620
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202 ggacagggcc tcttctcctg ctttcccata ttggtggcag tggtgccaca ctgaacagag 1740
203 tggaagacat atgccaatgca gctacaccta ccggccctgg gacgccggag gacagggcat 1800
204 tgtcctcagt cagatacaac agcatttggg gccatggtac ctgcacacct aaaacactag 1860
205 gccacgcata tgatctgtag tcacatgact aagccaagag gaaggagcaa gactcaagac 1920
206 atgattgatg gatgttaaag tctagcctga tgagagggga agtggtgggg gagacatagc 1980
207 cccacatga ggacatacaa ctgggaaata ctgaaacttg ctgcctattg ggtatgctga 2040
208 ggcacacag acttacagaa gaagtggccc tccatagaca tgtgtagcat caaaacacaa 2100
209 aggcacacac ttcctgacgg atgccagctt gggcactgct gtctactgac cccaaccctt 2160
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212 caccaggtag agttgtacag gttgtacact gcaggagagt gcctggcaaa aagatcaaat 2340
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214 gcacaaaagc actatatgga ctggtaatgg ttcacaggtt cagagattac ccagtgaggc 2460
215 cttattcctc ctttcccccc aaaactgaca ctttgttag ccacctcccc acccacatac 2520
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217 atatgcccga gctatgcctt gtctcttgtt cctgtttgca tttcactggg agcttgact 2640
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220 atgtgtagac aagctctcgc tctgtcacc aggctggagt gcagtgggtc aatcatggtt 2820
221 cactgcagtc ttgacctttt gggtcgaagt gatcctccca cctcagcctc ctgagtagct 2880
222 gggaccatag gctcacaaca ccacacctgg caaatttgat tttttttttt tttttcagag 2940
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224 gcc 3003
227 <210> SEQ ID NO: 4
228 <211> LENGTH: 6
229 <212> TYPE: PRT
230 <213> ORGANISM: Homo sapiens
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240 <213> ORGANISM: Homo sapiens
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247 <210> SEQ ID NO: 6
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249 <212> TYPE: DNA
250 <213> ORGANISM: Artificial Sequence
252 <220> FEATURE:
253 <223> OTHER INFORMATION: Description of Artificial Sequence: Cloning primer
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262 <213> ORGANISM: Artificial Sequence
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272 <211> LENGTH: 799
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274 <213> ORGANISM: Homo sapiens
276 <400> SEQUENCE: 8
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281           20           25           30
283 Ile Glu Thr Pro Leu Pro Lys Lys Glu Leu Leu Leu Pro Gly Asn Asn
284           35           40           45
286 Arg Lys Val Tyr Glu Leu Ser Asn Val Gln Glu Asp Ser Gln Pro Met
287           50           55           60
289 Cys Tyr Ser Asn Cys Pro Asp Gly Gln Ser Thr Ala Lys Thr Phe Leu
290   65           70           75           80
292 Thr Val Tyr Trp Thr Pro Glu Arg Val Glu Leu Ala Pro Leu Pro Ser
293           85           90           95
295 Trp Gln Pro Val Gly Lys Asn Leu Thr Leu Arg Cys Gln Val Glu Gly
296           100          105          110
298 Gly Ala Pro Arg Ala Asn Leu Thr Val Val Leu Leu Arg Gly Glu Lys
299           115          120          125
301 Glu Leu Lys Arg Glu Pro Ala Val Gly Glu Pro Ala Glu Val Thr Thr
302           130          135          140
304 Thr Val Leu Val Arg Arg Asp His His Gly Ala Asn Phe Ser Cys Arg
305  145          150          155          160
307 Thr Glu Leu Asp Leu Arg Pro Gln Gly Leu Glu Leu Phe Glu Asn Thr
308           165          170          175
310 Ser Ala Pro Tyr Gln Leu Gln Thr Phe Val Leu Pro Ala Thr Pro Pro
311           180          185          190
313 Gln Leu Val Ser Pro Arg Val Leu Glu Val Asp Thr Gln Gly Thr Val
314           195          200          205
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317           210          215          220
319 Leu Ala Leu Gly Asp Gln Arg Leu Asn Pro Thr Val Thr Tyr Gly Asn
320  225          230          235          240

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RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:14; N Pos. 2315

Seq#:82; Xaa Pos. 12,77,78,79,80,145,146,147,155,156,157,158,159,160,161

Seq#:82; Xaa Pos. 162,163,268,269,279,282

Seq#:88; Xaa Pos. 12,77,78,79,80,81,132,145,146,147